

10/1/05

## SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 75%

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.

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# ALIGNMENTS

## RESULT 1

US-10-131-827-305  
 ; Sequence 305, Application US/10131827  
 ; Publication No. US20040009479A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgemuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES  
 ; FILE REFERENCE: 506612000120  
 ; CURRENT APPLICATION NUMBER: US/10/131,827  
 ; CURRENT FILING DATE: 2002-09-06  
 ; PRIOR APPLICATION NUMBER: US 10/006,290  
 ; PRIOR FILING DATE: 2001-10-22  
 ; PRIOR APPLICATION NUMBER: US 60/296,764  
 ; PRIOR FILING DATE: 2001-06-08  
 ; NUMBER OF SEQ ID NOS: 9090  
 ; SOFTWARE: Patent version 3.1  
 ; SEQ ID NO 305  
 ; LENGTH: 50  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-131-827-305

Query Match 5.7%; Score 50; DB 1; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 1.5;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 530 ACATCCCTTGAGTACTGAGCCGCTTAACTCATCTCTATCTGTC 579

DB 1 ACATCCCTTGAGTACTGAGCCGCTTAACTCATCTCTATCTGTC 50

## RESULT 2

US-10-131-827-1951  
 ; Sequence 1951, Application US/10131827  
 ; Publication No. US20040009479A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wohlgemuth, Jay  
 ; APPLICANT: Fry, Kirk  
 ; APPLICANT: Woodward, Robert  
 ; APPLICANT: Ly, Ngoc  
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN  
 ; FILE REFERENCE: 506612000120  
 ; CURRENT APPLICATION NUMBER: US/10/131,827

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C 258	20	2.3	20	1	US-10-672-866-103	Sequence 103, Appl	C 331	18.4	2.1	21	1	US-10-301-516-26	Sequence 26, Appl
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C 322	19	2.2	25	1	US-10-700-816-13	Sequence 13, Appl	C 395	17.2	2.0	22	1	US-09-904-463-7	Sequence 7, Appl
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Sequence 103, Appl	US-10-672-866-103	20	2.3	20	2.3	20	1	US-10-672-866-103	Sequence 103, Appl
Sequence 104, Appl	US-10-672-866-104	20	2.3	20	2.3	20	1	US-10-672-866-104	Sequence 104, Appl
Sequence 105, Appl	US-10-672-866-105	20	2.3	20	2.3	20	1	US-10-672-866-105	Sequence 105, Appl
Sequence 106, Appl	US-10-672-866-106	20	2.3	20	2.3	20	1	US-10-672-866-106	Sequence 106, Appl
Sequence 107, Appl	US-10-672-866-107	20	2.3	20	2.3	20	1	US-10-672-866-107	Sequence 107, Appl
Sequence 108, Appl	US-10-672-866-108	20	2.3	20	2.3	20	1	US-10-672-866-108	Sequence 108, Appl
Sequence 109, Appl	US-10-672-866-109	20	2.3	20	2.3	20	1	US-10-672-866-109	Sequence 109, Appl
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Sequence 115, Appl	US-10-672-866-115	20	2.3	20	2.3	20	1	US-10-672-866-115	Sequence 115, Appl
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Sequence 126, Appl	US-10-672-866-126	20	2.3	20	2.3	20	1	US-10-672-866-126	Sequence 126, Appl
Sequence 127, Appl	US-10-672-866-127	20	2.3	20	2.3	20	1	US-10-672-866-127	Sequence 127, Appl
Sequence 128, Appl	US-10-672-866-128	20	2.3	20	2.3	20	1	US-10-672-866-128	Sequence 128, Appl
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Sequence 206, Appl	US-10-672-866-206	20	2.3	20	2.3	20	1	US-10-672-866-206	Sequence 206, Appl
Sequence 207, Appl	US-10-672-866-207	20	2.3	20	2.3	20	1</		

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126	20	2.3	20	1	US-10-633-843-25	Sequence 25, Appli	Sequence 25, Appli
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128	20	2.3	20	1	US-10-633-843-27	Sequence 27, Appli	Sequence 27, Appli
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132	20	2.3	20	1	US-10-633-843-31	Sequence 31, Appli	Sequence 31, Appli
133	20	2.3	20	1	US-10-633-843-32	Sequence 32, Appli	Sequence 32, Appli
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149	20	2.3	20	1	US-10-633-843-48	Sequence 48, Appli	Sequence 48, Appli
150	20	2.3	20	1	US-10-633-843-49	Sequence 49, Appli	Sequence 49, Appli
151	20	2.3	20	1	US-10-633-843-50	Sequence 50, Appli	Sequence 50, Appli
152	20	2.3	20	1	US-10-633-843-51	Sequence 51, Appli	Sequence 51, Appli
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171	20	2.3	20	1	US-10-633-843-70	Sequence 70, Appli	Sequence 70, Appli
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175	20	2.3	20	1	US-10-633-843-74	Sequence 74, Appli	Sequence 74, Appli
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179	20	2.3	20	1	US-10-672-866-4	Sequence 4, Appli	Sequence 4, Appli

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:42:42 ; Search time 6 Seconds  
(without alignments)  
3.913 Million cell updates/sec

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Perfect score: 874  
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Scoring table: IDENTITY\_NUC  
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Searched: 633 seqs, 13433 residues

Total number of hits satisfying chosen parameters: 1266

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 637 summaries

Database : pubdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	50	5.7	50	1	Sequence 305, Appl
3	48	5.5	48	1	Sequence 1951, Ap
4	48	5.5	48	1	Sequence 27, Appl
5	46.4	5.3	48	1	Sequence 7, Appl
6	46.4	5.3	48	1	Sequence 28, Appl
7	42	4.8	42	1	Sequence 8, Appl
8	42	4.8	42	1	Sequence 11, Appl
9	42	4.8	42	1	Sequence 73, Appl
10	42	4.8	42	1	Sequence 11, Appl
11	41	4.7	41	1	Sequence 12, Appl
12	41	4.7	41	1	Sequence 74, Appl
13	41	4.7	41	1	Sequence 12, Appl
14	41	4.7	41	1	Sequence 74, Appl
15	35	4.0	35	1	Sequence 32, Appl
16	35	4.0	35	1	Sequence 72, Appl
17	35	4.0	35	1	Sequence 15, Appl
18	33.4	3.8	35	1	US-10-894-721-2
19	27	3.1	27	1	US-09-899-807-1
20	25	2.9	25	1	Sequence 1, Appl
21	25	2.9	25	1	Sequence 19040, A
22	25	2.9	25	1	Sequence 19041, A
23	25	2.9	25	1	Sequence 19042, A
24	25	2.9	25	1	Sequence 19043, A
25	25	2.9	25	1	Sequence 19044, A
26	25	2.9	25	1	Sequence 19045, A
27	25	2.9	25	1	Sequence 19046, A
28	25	2.9	25	1	Sequence 19047, A
29	25	2.9	25	1	Sequence 19048, A
30	25	2.9	25	1	Sequence 19049, A
31	25	2.9	25	1	Sequence 19050, A
32	25	2.9	25	1	Sequence 19051, A
33	25	2.9	25	1	Sequence 19052, A
34	25	2.9	25	1	Sequence 19053, A

34	25	2.9	25	1	US-10-956-157-19054	Sequence 19054, A
35	25	2.9	25	1	US-10-956-157-19055	Sequence 19055, A
36	25	2.9	25	1	US-10-956-157-19056	Sequence 19056, A
37	25	2.9	25	1	US-10-956-157-19057	Sequence 19057, A
38	25	2.9	25	1	US-10-956-157-19058	Sequence 19058, A
39	25	2.9	25	1	US-10-956-157-19059	Sequence 19059, A
40	25	2.9	25	1	US-10-956-157-19060	Sequence 19060, A
41	25	2.9	25	1	US-10-956-157-19061	Sequence 19061, A
42	25	2.9	25	1	US-10-956-157-19062	Sequence 19062, A
43	25	2.9	25	1	US-10-956-157-19063	Sequence 19063, A
44	25	2.9	25	1	US-10-956-157-134047	Sequence 134047, A
45	25	2.9	25	1	US-10-956-157-134183	Sequence 134183, A
46	25	2.9	25	1	US-10-956-157-134860	Sequence 134860, A
47	25	2.9	25	1	US-10-956-157-139055	Sequence 139055, A
48	25	2.9	25	1	US-10-956-157-139603	Sequence 139603, A
49	25	2.9	25	1	US-10-956-157-149298	Sequence 149298, A
50	25	2.9	25	1	US-10-956-157-149376	Sequence 149376, A
51	25	2.9	25	1	US-10-956-157-150718	Sequence 150718, A
52	25	2.9	25	1	US-10-956-157-156203	Sequence 156203, A
53	25	2.9	25	1	US-10-956-157-160696	Sequence 160696, A
54	25	2.9	25	1	US-10-956-157-171822	Sequence 171822, A
55	25	2.9	25	1	US-10-956-157-173368	Sequence 173368, A
56	25	2.9	25	1	US-10-956-157-182879	Sequence 182879, A
57	25	2.9	25	1	US-10-956-157-184849	Sequence 184849, A
58	25	2.9	25	1	US-10-956-157-188144	Sequence 188144, A
59	25	2.9	25	1	US-10-956-157-189649	Sequence 189649, A
60	25	2.9	25	1	US-10-956-157-196119	Sequence 196119, A
61	25	2.9	25	1	US-10-956-157-196500	Sequence 196500, A
62	25	2.9	25	1	US-10-956-157-196788	Sequence 196788, A
63	25	2.9	25	1	US-10-956-157-206018	Sequence 206018, A
64	25	2.9	25	1	US-10-956-157-213479	Sequence 213479, A
65	25	2.9	25	1	US-10-956-157-214062	Sequence 214062, A
66	25	2.9	25	1	US-10-956-157-224634	Sequence 224634, A
67	25	2.9	25	1	US-10-956-157-220621	Sequence 220621, A
68	25	2.9	25	1	US-10-956-157-221193	Sequence 221193, A
69	25	2.9	25	1	US-10-956-157-224177	Sequence 224177, A
70	25	2.9	25	1	US-10-956-157-228500	Sequence 228500, A
71	25	2.9	25	1	US-10-956-157-233553	Sequence 233553, A
72	25	2.9	25	1	US-10-956-157-239197	Sequence 239197, A
73	25	2.9	25	1	US-10-956-157-241982	Sequence 241982, A
74	25	2.9	25	1	US-10-956-157-242800	Sequence 242800, A
75	25	2.9	25	1	US-10-956-157-247393	Sequence 247393, A
76	25	2.9	25	1	US-10-956-157-257204	Sequence 257204, A
77	25	2.9	25	1	US-10-956-157-259305	Sequence 259305, A
78	25	2.9	25	1	US-10-956-157-261942	Sequence 261942, A
79	25	2.9	25	1	US-10-956-157-266239	Sequence 266239, A
80	25	2.9	25	1	US-10-956-157-287005	Sequence 287005, A
81	24.4	2.8	32	1	US-11-070-868-4	Sequence 4, Appli
82	23.4	2.7	25	1	US-10-956-157-246110	Sequence 246110, A
83	23.4	2.7	25	1	US-10-956-157-277195	Sequence 277195, A
84	23	2.6	23	1	US-09-899-807-3	Sequence 3, Appli
85	23	2.6	23	1	US-09-899-807-4	Sequence 4, Appli
86	23	2.6	23	1	US-10-487-091-5	Sequence 5, Appli
87	23	2.6	23	1	US-10-487-091-6	Sequence 6, Appli
88	22.6	2.6	30	1	US-09-918-421-7	Sequence 7, Appli
89	22.4	2.6	25	1	US-10-719-900-61538	Sequence 61538, A
90	22.2	2.5	27	1	US-10-333-578-13	Sequence 13, Appl
91	22	2.5	27	1	US-10-333-578-12	Sequence 12, Appl
92	21.8	2.5	21	1	US-10-719-956-119457	Sequence 119457, A
93	21	2.4	21	1	US-10-109-349A-52	Sequence 52, Appl
94	21	2.4	21	1	US-10-103-349A-53	Sequence 53, Appl
95	21	2.4	21	1	US-10-633-843-6	Sequence 6, Appli
96	21	2.4	21	1	US-10-672-866-6	Sequence 6, Appli
97	21	2.4	21	1	US-10-719-900-826010	Sequence 826010, A
98	20.8	2.4	25	1	US-10-719-900-61537	Sequence 61537, A
99	20.4	2.3	25	1	US-10-719-900-456063	Sequence 456063, A
100	20.2	2.3	25	1	US-10-719-900-284833	Sequence 284833, A
101	20.2	2.3	25	1	US-10-719-900-458198	Sequence 458198, A
102	20.2	2.3	25	1	US-10-719-900-458199	Sequence 458199, A
103	20.2	2.3	25	1	US-10-719-900-889725	Sequence 889725, A
104	20.2	2.3	25	1	US-10-719-900-889726	Sequence 889726, A
105	20.2	2.3	25	1	US-10-719-900-893797	Sequence 893797, A
106	20.2	2.3	25	1	US-10-719-900-967669	Sequence 967669, A

*Published - Applications - NA*

ID ABZ00314 standard; DNA; 50 BP.  
 XX AC ABZ00314;  
 XX DT 09-JAN-2003 (first entry)  
 XX DE Human leukocyte gene expression profiling probe SEQ ID NO 305.  
 XX KW T7; leukocyte; gene expression profiling; allograft rejection;  
 XX KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
 XX KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; probe;  
 XX KW ss.  
 XX OS Homo sapiens.  
 XX XX WO200257414-A2.  
 XX PD 25-JUL-2002.  
 XX PF 22-OCT-2001; 2001WO-US047856.  
 XX PR 20-OCT-2000; 2000US-0241994P.  
 XX PR 08-JUN-2001; 2001US-0296764P.  
 XX XX (BIOC-) BIOCARDIA INC.  
 XX PI Wohlgenuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
 XX PI Ly N, Woodward R, Quettermous T, Johnson F;  
 XX DR WPI; 2002-636525/68.  
 XX XX New system for leukocyte expression profiling, diagnosing a disease, or  
 XX PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
 XX PT or congestive heart failure, comprises diagnostic oligonucleotides.  
 XX PS Claim 1; Page 336; Opp; English.  
 XX CC The invention relates to a system for detecting gene expression, which  
 XX CC comprises one or two isolated DNA molecules that detect expression of a  
 XX CC gene, where the gene corresponds to any of 8143 oligonucleotides  
 XX CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
 XX CC for leukocyte expression profiling. It is particularly useful for  
 XX CC diagnosing a disease, monitoring (rate of) progression of a disease,  
 XX CC predicting therapeutic outcome, determining prognosis for a patient,  
 XX CC predicting disease complications in an individual or monitoring response  
 XX CC to treatment in an individual. The diseases include cardiac allograft  
 XX CC rejection, kidney allograft rejection, liver allograft rejection,  
 XX CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
 XX CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection  
 XX SQ Sequence 50 BP; 9 A; 15 C; 9 G; 17 T; 0 U; 0 Other;  
 Query Match 5.7%; Score 50; DB 1; Length 50;  
 Best Local Similarity 100.0%; Pred. No. 0.042;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0  
 QY 530 ACATTCCTTGGATGTAGTCTGAGGCCCTTAATCTATCTGTTATCTGTCG 579  
 Db 1 ACATTCCTTGGATGTAGTCTGAGGCCCTTAATCTATCTGTTATCTGTCG 50  
 RESULT 2  
 ABZ01960  
 ID ABZ01960 standard; DNA; 50 BP.  
 XX AC ABZ01960;  
 XX DT 09-JAN-2003 (first entry)  
 XX DE Human leukocyte gene expression profiling probe SEQ ID NO 1951.  
 XX KW T7; leukocyte; gene expression profiling; allograft rejection;  
 XX KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
 XX KW KW

399	13.4	1.5	16	1	ADJ92751	Bacillus cereus sp	C 472	12.8	1.5	17	1	AAF06352	Hammerhead ribozym
C 400	13.4	1.5	17	1	AA74883	Mouse flt-1 VEGF r	C 473	12.8	1.5	17	1	AAF04741	Hammerhead ribozym
401	13.4	1.5	17	1	AA74883	Human KDR VEGF rec	474	12.8	1.5	17	1	AAF04741	Hammerhead ribozym
C 402	13.4	1.5	17	1	AA71528	Human KDR VEGF rec	C 475	12.8	1.5	17	1	AAF06353	Hammerhead ribozym
C 403	13.4	1.5	17	1	AA74882	Mouse flt-1 VEGF r	C 476	12.8	1.5	17	1	ABK01327	Human NOGO Inozyme
C 404	13.4	1.5	17	1	AA74882	Potato citrate syn	C 477	12.8	1.5	17	1	ABK02166	Human NOGO DNazyme
C 405	13.4	1.5	17	1	AA74882	Hammerhead ribozym	C 478	12.8	1.5	17	1	ABK02166	APC mutation corr
C 406	13.4	1.5	17	1	AA74882	Human NOGO Hammerh	C 479	12.8	1.5	17	1	ABK02166	LDLR mutation corr
C 407	13.4	1.5	17	1	ABK00398	MSH2 mutation corr	480	12.8	1.5	17	1	ABA80972	APC mutation corr
C 408	13.4	1.5	17	1	ABA80441	MSH2 mutation corr	481	12.8	1.5	17	1	ABA80972	LDLR mutation corr
C 409	13.4	1.5	17	1	ABA80441	Tumour suppression	C 482	12.8	1.5	17	1	ABA80973	Adenosine deaminas
410	13.4	1.5	17	1	ABT38905	Tumour suppression	C 483	12.8	1.5	17	1	ABA77178	Adenosine deaminas
411	13.4	1.5	17	1	ABT38905	Tumour suppression	C 484	12.8	1.5	17	1	ABT38905	Haemorrhagic Esche
412	13.4	1.5	17	1	ABT35779	Tumour suppression	C 485	12.8	1.5	17	1	ABL54647	Human p53AIP1 asso
C 413	13.4	1.5	17	1	ABT34906	Tumour suppression	C 486	12.8	1.5	17	1	ABL54647	Human p53AIP1 asso
C 414	13.4	1.5	17	1	ACD64073	HCV minus strand D	C 487	12.8	1.5	17	1	ABN01599	Human GDMPL-1 17-m
415	13.4	1.5	17	1	ACD60389	HCV DNazyme substr	C 488	12.8	1.5	17	1	ABN01599	Human GDMPL-1 17-m
416	13.4	1.5	17	1	ACD58596	HCV DNazyme substr	C 489	12.8	1.5	17	1	ABN01599	Human GDMPL-1 17-m
417	13.4	1.5	17	1	ACD62280	HCV minus strand D	C 490	12.8	1.5	17	1	ABN01598	Human GDMPL-1 17-m
418	13.4	1.5	17	1	ADB44863	Tumour suppression	C 491	12.8	1.5	17	1	ABN08969	Human GDMPL-1 17-m
C 419	13.4	1.5	17	1	ADJ50752	Human tumour suppr	C 492	12.8	1.5	17	1	ABN08969	Human GDMPL-1 17-m
C 420	13.4	1.5	17	1	ADJ50925	Human PTGDR substr	C 493	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
421	13.4	1.5	17	1	ADJ50925	HCV DNazyme substr	C 494	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
422	13.4	1.5	17	1	ADJ50925	HCV DNazyme substr	C 495	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
423	13.4	1.5	17	1	ADJ50925	Anti-SOD-1 295 cod	C 496	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
424	13.4	1.5	17	1	ADJ50925	Anti-SOD-1 359 cod	C 497	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
425	13.4	1.5	17	1	ADJ50925	Anti-SOD-1 186 cod	C 498	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
426	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 499	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 427	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 500	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 428	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 501	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 429	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 502	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 430	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 503	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 431	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 504	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 432	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 505	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 433	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 506	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 434	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 507	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 435	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 508	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 436	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 509	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 437	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 510	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 438	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 511	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 439	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 512	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 440	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 513	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 441	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 514	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 442	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 515	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 443	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 516	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 444	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 517	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 445	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 518	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 446	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 519	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 447	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 520	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 448	13.4	1.5	17	1	ADJ50925	Oligonucleotide SE	C 521	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 449	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 522	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 450	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 523	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 451	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 524	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 452	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 525	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 453	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 526	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 454	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 527	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 455	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 528	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 456	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 529	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 457	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 530	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 458	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 531	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 459	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 532	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 460	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 533	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 461	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 534	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 462	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 535	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 463	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 536	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 464	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 537	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 465	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 538	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 466	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 539	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 467	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 540	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 468	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 541	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 469	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 542	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 470	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 543	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m
C 471	12.8	1.5	16	1	ADJ50925	Oligonucleotide SE	C 544	12.8	1.5	17	1	ABN07230	Human GDMPL-1 17-m



c 253	16	1.8	17	1	AAF91027	Human multi drug r	c 326	14.4	1.6	17	1	ADB88284	Human UGT1A1 varia
254	16	1.8	17	1	ADI50808	Human tumour suppr	c 327	14.4	1.6	17	1	ADB97267	Human MDR1 variant
255	16	1.8	17	1	ADI50799	Human tumour suppr	c 328	14.4	1.6	17	1	ADB97268	Human MDR1 variant
c 256	16	1.8	18	1	ABK41012	Human obesity-asso	c 329	14.4	1.6	17	1	ADB92459	Human MDR1 variant
257	16	1.8	19	1	AA150752	PAL/alpha-tubulin-	c 330	14.4	1.6	17	1	ADB92458	Human MDR1 variant
258	16	1.8	19	1	ADM83390	Coffea arabica PAL	c 331	14.4	1.6	17	1	ADB44992	Tumour suppression
c 259	15.8	1.8	20	1	AA153235	Anticsease oligonuc	c 332	14.4	1.6	17	1	AD148262	Human tumour suppr
c 260	15.8	1.8	20	1	AAV85741	LRP5 exon primer E	c 333	14.4	1.6	17	1	ABZ76052	Antigene inhibitin
c 261	15.8	1.8	20	1	ACC44079	Oligo ISIS 124670	c 334	14.4	1.6	18	1	ABZ76052	Primer of the inve
c 262	15.8	1.8	20	1	ADL59647	Human ESM-1 antise	c 335	14.4	1.6	18	1	AAZ32081	Xylulokinase PCR p
c 263	15.8	1.8	20	1	ADL59286	Human ESM-1 antise	c 336	14.4	1.6	19	1	AAH83961	Cyclin A2 ribozyme
c 264	15.8	1.8	21	1	AAV72769	Corn kernel oil co	c 337	14.4	1.6	19	1	AAH59123	Cyclin A2 ribozyme
c 265	15.8	1.8	21	1	ABZ98130	Human multdrug re	c 338	14.4	1.6	19	1	ADR77596	Human apolipoprote
266	15.6	1.8	17	1	ACF62527	Cancer based on CY	c 339	14.4	1.6	19	1	ADR79231	Human apolipoprote
267	15.6	1.8	17	1	ADB21198	MRP1 based cancer	c 340	14.4	1.6	19	1	ADR74990	Common primer for
268	15.6	1.8	17	1	ADB88287	Human UGT1A1 varia	341	14	1.6	17	1	AAH81501	Human c-myb hamme
269	15.6	1.8	17	1	ADB97270	Human MDR1 variant	342	14	1.6	17	1	AAH81503	Human c-myb hamme
270	15.6	1.8	17	1	ADB92461	Human MDR1 variant	343	14	1.6	17	1	AAH81500	Human c-myb hamme
c 271	15.4	1.8	17	1	AAAF03382	Hammerhead ribozym	344	14	1.6	17	1	AAH81502	Human c-myb hamme
c 272	15.4	1.8	17	1	AAAF03383	Hammerhead ribozym	c 345	14	1.6	17	1	ABK01349	Human NOGO Inozyme
c 273	15.4	1.8	20	1	ADI81744	Human protein kina	c 346	14	1.6	17	1	ABK00484	Human NOGO Hammerh
274	15.4	1.8	20	1	ADI81684	Human protein kina	c 347	14	1.6	17	1	ABK01996	Human NOGO Zinzyne
c 275	15.2	1.7	20	1	AAH08640	Primer for amplify	348	14	1.6	17	1	ACA08316	Necrosis factor ka
c 276	15.2	1.7	20	1	AAH08640	Human STAT3 phosph	349	14	1.6	17	1	ACA09130	NFKB sub-unit modu
c 277	15.2	1.7	20	1	AAH33188	Human STAT3 phosph	350	14	1.6	20	1	ACC40921	Human superoxide d
278	15.2	1.7	20	1	AAH57024	Human oestrogen re	351	14	1.6	20	1	ACC40922	Human superoxide d
279	15.2	1.7	20	1	ABQ99746	Human STAT3 antise	c 352	13.8	1.6	17	1	AAH73200	Mouse fix-1 VEGF r
c 280	15.2	1.7	20	1	ABZ24780	Deoxyuridine monop	353	13.8	1.6	17	1	AAV96545	Potato citrate syn
281	15.2	1.7	20	1	ACF39665	MHC class II trans	354	13.8	1.6	17	1	AAV04937	Hammerhead ribozym
282	15.2	1.7	20	1	ADB99942	Vitamin D nuclear	355	13.8	1.6	17	1	AAV04936	Hammerhead ribozym
283	15.2	1.7	20	1	ADFI7531	Rhodotorula glutin	356	13.8	1.6	17	1	AAV04935	Hammerhead ribozym
284	15.2	1.7	20	1	ABZ30760	Human oligonucleot	c 357	13.8	1.6	17	1	ABK01097	Human NOGO Inozyme
285	15.2	1.7	20	1	ABZ90984	Human oligonucleot	c 358	13.8	1.6	17	1	ABA80297	MLH1 mutation corr
286	15.2	1.7	20	1	ABD26990	H93087-derived oli	359	13.8	1.6	17	1	ABA80296	Human multi drug r
287	15.2	1.7	20	1	ABD27214	AA180912-derived o	c 360	13.8	1.6	17	1	AAV91029	Human GMPLP-1 17-m
c 288	15.2	1.7	20	1	ADL59322	Human ESM-1 antise	361	13.8	1.6	17	1	ABN08968	WNV Zinzyne subetr
c 289	15.2	1.7	20	1	ADL59256	Human ESM-1 antise	362	13.8	1.6	17	1	ACN03785	Human MDZ7 scannin
c 290	15.2	1.7	20	1	ADK11305	Set 1 right PCR pr	363	13.8	1.6	17	1	ACD02281	HCV minus strand D
c 291	15.2	1.7	20	1	ADK21489	Acyl-coenzyme A sy	364	13.8	1.6	17	1	ADF62659	Human PCP1 DNA fr
292	15.2	1.7	20	1	ADR70258	Human apoptosis-sp	c 365	13.8	1.6	17	1	ADL51188	Human PTGDR subetr
293	15	1.7	15	1	AAH71205	Sequence of probe	c 366	13.8	1.6	17	1	ADL51187	Human PTGDR subetr
294	15	1.7	15	1	AAQ61567	Human SOD probe.	c 367	13.8	1.6	17	1	ADL51156	Human PTGDR subetr
295	15	1.7	15	1	ADQ43600	Wild type DNA frag	c 368	13.8	1.6	17	1	ADL51536	HCV DNazyme subetr
296	15	1.7	15	1	ADQ43606	Wild type DNA frag	c 369	13.8	1.6	17	1	ADL51531	Human GMPLP-1 prob
297	15	1.7	17	1	AAH21294	Human MDR-1 allele	c 370	13.8	1.6	18	1	ACN72058	Primer #2 for eWSS
c 298	15	1.7	17	1	AAH21293	Human MDR-1 allele	c 371	13.8	1.6	18	1	AAH716415	Maize retinoblasto
c 299	15	1.7	17	1	AAH21293	Human multi drug r	c 372	13.8	1.6	18	1	AAV05715	Maize retinoblasto
300	15	1.7	17	1	ABT38676	Tumour suppression	c 373	13.8	1.6	18	1	AAV17082	PCR primer used to
c 301	15	1.7	17	1	ACF62526	Cancer based on CY	c 374	13.8	1.6	18	1	AAH85777	Human OB gene sequ
c 302	15	1.7	17	1	ADB21197	MRP1 based cancer	c 375	13.8	1.6	18	1	AAH86600	Cdc 2 kinase hamme
c 303	15	1.7	17	1	ADB88286	Human UGT1A1 varia	c 376	13.8	1.6	18	1	AAH86600	Cdc 2 kinase hamme
c 304	15	1.7	17	1	ADB97269	Human MDR1 variant	c 377	13.8	1.6	18	1	AAH86600	Human Ets-2 phosph
c 305	15	1.7	17	1	ADB92460	Human MDR1 variant	c 378	13.8	1.6	18	1	AAH86600	Human OB DNA PCR p
c 306	15	1.7	20	1	AAV13337	Anticsease primer E	c 379	13.8	1.6	18	1	AAH86600	Burkholderia cepac
c 307	14.8	1.7	19	1	AAV72612	Glucose-6-phosphat	c 380	13.8	1.6	18	1	AAH86600	Human OB gene sequ
c 308	14.8	1.7	19	1	AAH82988	Cdk6 ribozyme bind	c 381	13.8	1.6	18	1	AAH86600	Cdc 2 kinase hamme
c 309	14.8	1.7	19	1	AAH85150	Cell-cycle depende	c 382	13.8	1.6	18	1	ABX89564	Human sequence tag
c 310	14.8	1.7	19	1	ADH01862	Protein tyrosine p	c 383	13.8	1.6	18	1	ABL61438	Human Ob gene STS
c 311	14.8	1.7	19	1	ADM34090	Mouse RIKEN 492151	c 384	13.8	1.6	18	1	ABZ10441	Haematopoietic cel
c 312	14.8	1.7	19	1	AAH80828	Human glucose-6-ph	c 385	13.8	1.6	18	1	ABX96424	Human obese (ob) g
c 313	14.4	1.6	17	1	AAH23007	Integrin subunit b	c 386	13.8	1.6	18	1	ADH84339	Primer oligo used
c 314	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 387	13.8	1.6	18	1	ADH84339	Human lymphoid cel
c 315	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 388	13.8	1.6	18	1	ADH84339	Chromosomal abnorm
c 316	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 389	13.8	1.6	18	1	ADH84339	Human APC (adenoma
c 317	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 390	13.8	1.6	18	1	ADH84339	Human APC DNA frag
c 318	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 391	13.8	1.6	18	1	ADH84339	Human APC DNA frag
c 319	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 392	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
c 320	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 393	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
c 321	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 394	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
c 322	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 395	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
c 323	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 396	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
c 324	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 397	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
325	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 398	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
326	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 399	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
327	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 400	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
328	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 401	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
329	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 402	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
330	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 403	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
331	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 404	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
332	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 405	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
333	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 406	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
334	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 407	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
335	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 408	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
336	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 409	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
337	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 410	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
338	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 411	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
339	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 412	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
340	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 413	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
341	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 414	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
342	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 415	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
343	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 416	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
344	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 417	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
345	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 418	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
346	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 419	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
347	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 420	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
348	14.4	1.6	17	1	AAH05438	Hammerhead ribozym	c 421	13.8	1.6	18	1	ADH84339	IGF-I oligonucleot
349	14.4	1.6	17	1	AAH05438	Hammerhead ribozym							

C 107	20	2.3	20	1	ACCA0927	Human superoxide d	C 180	17.2	2.0	22	1	ACD23495	Human PRO PCR prim
C 108	20	2.3	20	1	ADQ80681	Human cytosolic su	C 181	17.2	2.0	22	1	ADB77533	Human secreted/tra
C 109	20	2.3	20	1	ADR42714	SOD gene analysis	C 182	17.2	2.0	22	1	ADB74669	Human secreted/tra
C 110	20	2.3	20	1	ADR42715	SOD gene analysis	C 183	17.2	2.0	22	1	ADC28315	Human secreted/tra
C 111	20	2.3	21	1	AAQ67477	PCR primer for hum	C 184	17.2	2.0	22	1	ADC28315	Human secreted/tra
C 112	20	2.3	21	1	AAQ67477	Human SOD1 exon 1	C 185	17.2	2.0	22	1	ADC40029	Human secreted/tra
C 113	20	2.3	21	1	AAV73827	Human cytosolic su	C 186	17.2	2.0	22	1	ADC18857	Human secreted/tra
C 114	20	2.3	25	1	ADQ43049	Short interfering	C 187	17.2	2.0	22	1	ADC34153	Human secreted/tra
C 115	19.8	2.3	23	1	ABQ75418	CuZn superoxide di	C 188	17.2	2.0	22	1	ADC29208	Human secreted/tra
C 116	19.4	2.2	21	1	ADQ52404	Target DNA sequenc	C 189	17.2	2.0	22	1	ADC28739	Human secreted/tra
C 117	19.4	2.2	21	1	ADQ52403	Target DNA sequenc	C 190	17.2	2.0	22	1	ADC40624	Human secreted/tra
C 118	19.4	2.2	22	1	AAH81808	Probe used to iden	C 191	17.2	2.0	22	1	ADC19281	Human secreted/tra
C 119	19.4	2.2	25	1	ADQ43051	Short interfering	C 192	17.2	2.0	22	1	ADC33729	Human secreted/tra
C 120	19.2	2.2	23	1	ADQ52415	siRNA p9 sequence	C 193	17.2	2.0	22	1	ADC12799	Human secreted/tra
C 121	19.2	2.2	23	1	ADQ52417	siRNA p11 sequence	C 194	17.2	2.0	22	1	ADC12251	Human secreted/tra
C 122	19	2.2	19	1	AAH60181	Sequence of probe	C 195	17.2	2.0	22	1	ADD04806	Human secreted/tra
C 123	19	2.2	19	1	ABQ73056	Cu/Zn SOD gene rel	C 196	17.2	2.0	22	1	ADD03812	Human secreted/tra
C 124	19	2.2	19	1	ADQ80680	Human cytosolic su	C 197	17.2	2.0	22	1	ADD03388	Human secreted/tra
C 125	19	2.2	23	1	ADQ52425	siRNA p11 sequence	C 198	17.2	2.0	22	1	ADQ34640	Human secreted/tra
C 126	19	2.2	23	1	ADQ52424	siRNA p10 sequence	C 199	17.2	2.0	22	1	ADH59123	Human secreted/tra
C 127	19	2.2	23	1	ADQ52423	siRNA p9 sequence	C 200	17.2	2.0	22	1	ADH59123	Human secreted/tra
C 128	19	2.2	25	1	ADQ43052	Short interfering	C 201	17.2	2.0	22	1	ADH59123	Human secreted/tra
C 129	19	2.2	25	1	ADQ43053	Short interfering	C 202	17.2	2.0	22	1	ACA58900	Human secreted/tra
C 130	19	2.2	25	1	ADQ43050	Short interfering	C 203	17.2	2.0	22	1	ACA58900	Human secreted/tra
C 131	19	2.2	25	1	ADQ43054	Short interfering	C 204	17.2	2.0	22	1	ACA58900	Human secreted/tra
C 132	18.4	2.1	20	1	AAV01384	Superoxide dismuta	C 205	17.2	2.0	22	1	ACA58900	Human secreted/tra
C 133	18.2	2.1	24	1	ADD26381	RT-PCR primer #2 f	C 206	17.2	2.0	22	1	ACA58900	Human secreted/tra
C 134	18	2.1	18	1	ADQ76694	PCR primer for CuZ	C 207	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 135	18	2.1	23	1	ADQ52416	siRNA p10 sequence	C 208	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 136	18	2.1	23	1	ADQ52411	Mutant siRNA p10 s	C 209	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 137	17.6	2.0	23	1	ADQ52410	Mutant siRNA p11 s	C 210	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 138	17.6	2.0	23	1	ADQ52412	Mutant siRNA p9 se	C 211	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 139	17.4	2.0	19	1	ADQ52401	Target DNA sequenc	C 212	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 140	17.4	2.0	19	1	ADQ52402	Target DNA sequenc	C 213	17.2	2.0	22	1	ADH73185	Human secreted/tra
C 141	17.4	2.0	20	1	ABD28123	Human oligonucleot	C 214	17.2	2.0	22	1	ADG92103	Human secreted/tra
C 142	17.4	2.0	20	1	ABD28123	AA156940-derived o	C 215	17.2	2.0	22	1	ADG92530	Human secreted/tra
C 143	17.4	2.0	21	1	ABD28129	Human multidrug re	C 216	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 144	17.4	2.0	23	1	ADQ52421	Mutant siRNA p10 s	C 217	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 145	17.4	2.0	23	1	ADQ52420	Mutant siRNA p11 s	C 218	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 146	17.4	2.0	23	1	ADQ52422	Mutant siRNA p9 se	C 219	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 147	17.2	2.0	22	1	AAQ28452	EGF-like/FGF-8 hom	C 220	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 148	17.2	2.0	22	1	AAQ28452	Human PRO217 prime	C 221	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 149	17.2	2.0	22	1	AAQ28452	Primer 28730.r (OL	C 222	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 150	17.2	2.0	22	1	AAQ28452	Primer for amplify	C 223	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 151	17.2	2.0	22	1	AAQ28452	Reverse PCR primer	C 224	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 152	17.2	2.0	22	1	AAQ28452	Reverse primer 287	C 225	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 153	17.2	2.0	22	1	AAQ28452	Primer for amplify	C 226	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 154	17.2	2.0	22	1	AAQ28452	Human PRO protein-	C 227	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 155	17.2	2.0	22	1	AAQ28452	Human PRO oligonuc	C 228	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 156	17.2	2.0	22	1	AAQ28452	PCR primer 4 for H	C 229	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 157	17.2	2.0	22	1	AAQ28452	Human PRO211 PCR p	C 230	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 158	17.2	2.0	22	1	AAQ28452	PRO211 reverse PCR	C 231	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 159	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 232	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 160	17.2	2.0	22	1	AAQ28452	Secreted and trans	C 233	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 161	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 234	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 162	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 235	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 163	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 236	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 164	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 237	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 165	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 238	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 166	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 239	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 167	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 240	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 168	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 241	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 169	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 242	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 170	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 243	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 171	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 244	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 172	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 245	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 173	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 246	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 174	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 247	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 175	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 248	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 176	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 249	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 177	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 250	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 178	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 251	17.2	2.0	22	1	ADH20319	Human secreted/tra
C 179	17.2	2.0	22	1	AAQ28452	Human secreted/tra	C 252	17.2	2.0	22	1	ADH20319	Human secreted/tra

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:44:11 ; Search time 6 Seconds  
(without alignments)  
3.425 Million cell updates/sec

Title: US-10-633-843-3-COPY

Perfect score: 874

Sequence: 1 ctgcagctcgggtttcc.....tattaaagaatccaaattc 874

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 0.5

Searched: 608 seqs, 11755 residues

Total number of hits satisfying chosen parameters: 1216

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 610 summaries

Database : ngsdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

*N. Geneseg*

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	5.7	50	1	ABZ00314 Human leukocyte ge
2	50	5.7	50	1	ABZ01960 Human leukocyte ge
3	48	5.5	48	1	AD52413 Wild-type human SO
4	48	5.5	48	1	ADO43047 Superoxide dismuta
5	46.4	5.3	48	1	AD52414 Human SOD1 mutant
6	46.4	5.3	48	1	ADO43048 Superoxide dismuta
7	40	4.6	40	1	AAQ27817 Primer AO39. Synt
8	35	4.0	35	1	AD52418 Wild-type human SO
9	35	4.0	35	1	ADO43055 Superoxide dismuta
10	28	3.2	28	1	ABK66923 Human gene specifi
11	28	3.2	28	1	ABK66924 Human gene specifi
12	27	3.1	27	1	ABA94683 Antisense S-oligo
13	25	2.9	33	1	ADQ75020 Human superoxide d
14	24	2.7	24	1	AAQ67485 PCR primer for hum
15	24	2.7	24	1	AAV73935 Human SOD1 exon 5
16	24	2.7	24	1	ADO55698 Human cytosolic su
17	23	2.6	23	1	ABA94686 Superoxide dismuta
18	23	2.6	23	1	ABA94685 Superoxide dismuta
19	23	2.6	23	1	ABX12365 Oxidative stress d
20	23	2.6	23	1	ABX12364 Oxidative stress d
21	22.6	2.6	30	1	AA888339 Mouse (balb/c) for
22	22.6	2.6	30	1	AA888339 Mouse Cu/Zn-SOD (s
23	22.4	2.6	25	1	AAQ13501 Rat superoxide dis
24	22.2	2.5	27	1	AAQ29666 Human Zn-SOD ampli
25	22.2	2.5	27	1	ADO59161 Human Cu/Zn-supero
26	22.2	2.5	27	1	ADO06573 Fusion protein rel
27	22.2	2.5	27	1	ADO74975 Tat-pyridoxal kina
28	22	2.5	22	1	ADG73925 Human superoxide d
29	22	2.5	22	1	ADG73926 Human superoxide d
30	22	2.5	27	1	ADO59160 Human Cu/Zn-supero
31	22	2.5	27	1	ADO06572 Fusion protein rel
32	22	2.5	27	1	ADO74974 Tat-pyridoxal kina
33	22	2.5	29	1	AAV32582 Human SOD-1 cDNA P

C	34	21	2.4	21	1	ABQ73054 Cu/Zn SOD gene rel
C	35	21	2.4	21	1	ABZ79578 Human superoxide d
C	36	21	2.4	21	1	ADD56532 Human gene express
C	37	21	2.4	21	1	ADD56533 Human gene express
C	38	21	2.4	21	1	ADT66493 PCR primer for Cu2
C	39	20.4	2.3	20	1	Cu/Zn SOD gene rel
C	40	20	2.3	20	1	Superoxide dismuta
C	41	20	2.3	20	1	Human superoxide d
C	42	20	2.3	20	1	Human superoxide d
C	43	20	2.3	20	1	Human superoxide d
C	44	20	2.3	20	1	Human superoxide d
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C	103	20	2.3	20	1	Human superoxide d
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C	105	20	2.3	20	1	Human superoxide d
C	106	20	2.3	20	1	Human superoxide d

c 107	13.4	1.5	17	1	US-08-584-040-7633	Sequence 7633, Ap
c 108	13.4	1.5	17	1	US-09-371-772B-2045	Sequence 2045, Ap
c 109	13.4	1.5	17	1	US-09-371-772B-2046	Sequence 2046, Ap
c 110	13.4	1.5	17	1	US-09-371-772B-3424	Sequence 3424, Ap
c 111	13.4	1.5	17	1	US-09-371-772B-3425	Sequence 3425, Ap
c 112	13.4	1.5	17	1	US-09-685-664B-2045	Sequence 2045, Ap
c 113	13.4	1.5	17	1	US-09-685-664B-2046	Sequence 2046, Ap
c 114	13.4	1.5	17	1	US-09-685-664B-3424	Sequence 3424, Ap
c 115	13.4	1.5	17	1	US-09-685-664B-3425	Sequence 3425, Ap
c 116	13	1.5	16	1	US-09-371-772B-7004	Sequence 7004, Ap
c 117	13	1.5	17	1	US-08-584-040-1903	Sequence 1903, Ap
c 118	13	1.5	17	1	US-09-371-772B-448	Sequence 448, Ap
c 119	13	1.5	17	1	US-09-371-772B-4718	Sequence 4718, Ap
c 120	13	1.5	17	1	US-09-371-772B-6292	Sequence 6292, Ap
c 121	13	1.5	17	1	US-09-371-772B-6293	Sequence 6293, Ap
c 122	13	1.5	17	1	US-09-685-664B-448	Sequence 448, Ap
c 123	12.8	1.5	16	1	US-09-371-772B-5969	Sequence 5969, Ap
c 124	12.8	1.5	16	1	US-09-371-772B-6103	Sequence 6103, Ap
c 125	12.8	1.5	17	1	US-08-985-162-718	Sequence 718, Ap
c 126	12.8	1.5	17	1	US-08-606-505B-52	Sequence 52, Appl
c 127	12.8	1.5	17	1	US-09-616-990-52	Sequence 52, Appl
c 128	12.8	1.5	17	1	US-08-584-040-2663	Sequence 2663, Ap
c 129	12.8	1.5	17	1	US-08-584-040-5361	Sequence 5361, Ap
c 130	12.8	1.5	17	1	US-08-584-040-7274	Sequence 7274, Ap
c 131	12.8	1.5	17	1	US-08-584-040-7916	Sequence 7916, Ap
c 132	12.8	1.5	17	1	US-09-371-772B-1207	Sequence 1207, Ap
c 133	12.8	1.5	17	1	US-09-371-772B-2263	Sequence 2263, Ap
c 134	12.8	1.5	17	1	US-09-371-772B-3083	Sequence 3083, Ap
c 135	12.8	1.5	17	1	US-09-371-772B-3699	Sequence 3699, Ap
c 136	12.8	1.5	17	1	US-09-371-772B-4534	Sequence 4534, Ap
c 137	12.8	1.5	17	1	US-09-371-772B-5538	Sequence 5538, Ap
c 138	12.8	1.5	17	1	US-09-371-772B-6266	Sequence 6266, Ap
c 139	12.8	1.5	17	1	US-09-371-772B-6267	Sequence 6267, Ap
c 140	12.8	1.5	17	1	US-09-401-063-718	Sequence 718, Ap
c 141	12.8	1.5	17	1	US-09-866-108A-1590	Sequence 1590, Ap
c 142	12.8	1.5	17	1	US-09-866-108A-1591	Sequence 1591, Ap
c 143	12.8	1.5	17	1	US-09-866-108A-2708	Sequence 2708, Ap
c 144	12.8	1.5	17	1	US-09-866-108A-2709	Sequence 2709, Ap
c 145	12.8	1.5	17	1	US-09-866-108A-7221	Sequence 7221, Ap
c 146	12.8	1.5	17	1	US-09-866-108A-7222	Sequence 7222, Ap
c 147	12.8	1.5	17	1	US-09-866-108A-7767	Sequence 7767, Ap
c 148	12.8	1.5	17	1	US-09-866-108A-7768	Sequence 7768, Ap
c 149	12.8	1.5	17	1	US-09-866-108A-7981	Sequence 7981, Ap
c 150	12.8	1.5	17	1	US-09-866-108A-7982	Sequence 7982, Ap
c 151	12.8	1.5	17	1	US-09-866-108A-8159	Sequence 8159, Ap
c 152	12.8	1.5	17	1	US-09-866-108A-8160	Sequence 8160, Ap
c 153	12.8	1.5	17	1	US-09-866-108A-8959	Sequence 8959, Ap
c 154	12.8	1.5	17	1	US-09-866-108A-8961	Sequence 8961, Ap
c 155	12.8	1.5	17	1	US-09-866-108A-10213	Sequence 10213, A
c 156	12.8	1.5	17	1	US-09-866-108A-10214	Sequence 10214, A
c 157	12.8	1.5	17	1	US-09-404-912-470	Sequence 470, Ap
c 158	12.8	1.5	17	1	US-09-720-435A-30	Sequence 30, Appl
c 159	12.8	1.5	17	1	US-09-720-435A-191	Sequence 191, Appl
c 160	12.8	1.5	17	1	US-09-685-664B-1207	Sequence 1207, Ap
c 161	12.8	1.5	17	1	US-09-685-664B-2263	Sequence 2263, Ap
c 162	12.8	1.5	17	1	US-09-685-664B-3083	Sequence 3083, Ap
c 163	12.8	1.5	17	1	US-09-685-664B-3699	Sequence 3699, Ap
c 164	12.8	1.5	15	1	US-08-311-760A-197	Sequence 197, Appl
c 165	12.4	1.4	15	1	US-08-363-240A-144	Sequence 144, Appl
c 166	12.4	1.4	15	1	US-08-363-240A-145	Sequence 145, Appl
c 167	12.4	1.4	15	1	US-08-774-310-197	Sequence 197, Appl
c 168	12.4	1.4	15	1	US-09-531-000-9	Sequence 9, Appl
c 169	12.4	1.4	16	1	US-09-371-772B-5681	Sequence 5681, Ap
c 170	12	1.4	15	1	US-08-319-492B-148	Sequence 148, Appl
c 171	12	1.4	15	1	US-08-363-240A-143	Sequence 143, Appl
c 172	12	1.4	15	1	US-08-635-309-24	Sequence 24, Appl
c 173	12	1.4	15	1	US-08-585-684B-2103	Sequence 2103, Ap
c 174	12	1.4	15	1	US-09-038-073-2103	Sequence 31, Appl
c 175	12	1.4	16	1	US-08-173-489C-31	Sequence 31, Appl
c 176	12	1.4	16	1	US-09-371-772B-6963	Sequence 6963, Ap
c 177	12	1.4	17	1	US-08-373-124A-962	Sequence 962, Appl
c 178	12	1.4	17	1	US-08-373-124A-964	Sequence 964, Appl
c 179	12	1.4	17	1	US-08-373-124A-966	Sequence 966, Appl

ALIGNMENTS

RESULT 1

US-08-859-998-1011  
 ; Sequence 1011, Application US/08859998  
 ; Patent No. 5994076  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chenchik, Alex  
 ; APPLICANT: Jokhadze, George  
 ; APPLICANT: Bibilashvili, Robert  
 ; TITLE OF INVENTION: METHOD OF ASSAYING DIFFERENTIAL  
 ; TITLE OF INVENTION: EXPRESSION  
 ; NUMBER OF SEQUENCES: 1375  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESS: Fish & Richardson, P.C.  
 ; STREET: 2200 Sand Hill Road, Suite 100  
 ; CITY: Menlo Park  
 ; STATE: CA  
 ; COUNTRY: US  
 ; ZIP: 94025  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/859,998  
 ; FILING DATE: 21-MAY-1997  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Field, Bret E.  
 ; REGISTRATION NUMBER: 37,620  
 ; REFERENCE/DOCKET NUMBER: 09096/002001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-322-5070  
 ; TELEFAX: 415-854-0875  
 ; INFORMATION FOR SEQ ID NO: 1011:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 28 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; FEATURE:  
 ; OTHER INFORMATION: oligonucleotide primer  
 ; US-08-859-998-1011

Query Match 3.2%; Score 28; DB 1; Length 28;  
 Best Local Similarity 100.0%; Pred. No. 1.4;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 106 AGTCAGGCGCATCATTTTGGACGAG 133

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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:41:23 ; Search time 2 Seconds  
(without alignments)  
2.994 Million cell updates/sec

Title: US-10-633-843-3-COPY  
Perfect score: 874  
Sequence: 1 ctgcgagctctgggtttcc.....tattaaagaatccaaattc 874

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 0.5

Searched: 188 seqs, 3426 residues

Total number of hits satisfying chosen parameters: 376

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 194 summaries

Database : issdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	28	3.2	28	1	US-08-859-998-1011
2	28	3.2	28	1	US-08-859-998-1012
3	28	3.2	28	1	US-09-225-928-1011
4	28	3.2	28	1	US-09-225-928-1012
5	28	3.2	28	1	US-09-225-201B-1011
6	28	3.2	28	1	US-09-225-201B-1012
7	24	2.7	24	1	US-08-023-980B-18
8	24	2.7	24	1	US-08-486-953A-13
9	24	2.7	24	1	US-08-204-052-13
10	22	2.5	29	1	US-08-868-381A-2
11	21.8	2.5	25	1	5290690-19
12	21.8	2.5	25	1	5290690-19
13	20	2.3	21	1	US-08-023-980B-5
14	20	2.3	21	1	US-08-486-953A-5
15	20	2.3	21	1	US-08-204-052-5
16	17.2	2.0	22	1	US-09-907-794A-7
17	17.2	2.0	22	1	US-09-905-125A-7
18	17.2	2.0	22	1	US-09-302-775A-7
19	17.2	2.0	22	1	US-09-906-700-7
20	17.2	2.0	22	1	US-09-903-603A-7
21	17.2	2.0	22	1	US-09-304-920A-7
22	17.2	2.0	22	1	US-09-909-064-7
23	17.2	2.0	22	1	US-09-905-381A-7
24	17.2	2.0	22	1	US-09-906-618-7
25	17.2	2.0	22	1	5290690-20
26	17.2	2.0	22	1	5290690-20
27	17	1.9	21	1	US-08-023-980B-7
28	17	1.9	21	1	US-08-486-953A-7
29	17	1.9	21	1	US-08-204-052-7
30	16.8	1.9	20	1	US-09-068-506-48
31	16.8	1.9	21	1	US-08-023-980B-10
32	16.8	1.9	21	1	US-08-486-953A-10
33	16.8	1.9	21	1	US-08-204-052-10

34	16	1.8	19	1	US-09-545-686-27	Sequence 27, Appl
35	15.8	1.8	20	1	US-08-062-042-2	Sequence 2, Appl
36	15.8	1.8	20	1	US-09-060-299-236	Sequence 236, Appl
37	15.8	1.8	20	1	US-09-402-923A-236	Sequence 236, Appl
38	15.8	1.8	20	1	US-09-909-595-79	Sequence 79, Appl
39	15.2	1.7	20	1	US-09-040-285A-4	Sequence 4, Appl
40	15.2	1.7	20	1	US-09-288-461-39	Sequence 39, Appl
41	15.2	1.7	20	1	US-09-758-881-39	Sequence 39, Appl
42	15	1.7	20	1	US-08-846-020A-17	Sequence 17, Appl
43	15	1.7	20	1	US-09-617-871-17	Sequence 17, Appl
44	14.8	1.7	19	1	US-09-108-006C-31	Sequence 31, Appl
45	14.8	1.7	19	1	US-09-696-791-574	Sequence 574, Appl
46	14.4	1.6	17	1	US-08-412-614-102	Sequence 102, Appl
47	14.4	1.6	17	1	US-08-412-614-104	Sequence 104, Appl
48	14.4	1.6	17	1	US-08-635-761-102	Sequence 102, Appl
49	14.4	1.6	17	1	US-08-635-761-104	Sequence 104, Appl
50	14.4	1.6	17	1	US-09-312-520-102	Sequence 102, Appl
51	14.4	1.6	17	1	US-09-312-520-104	Sequence 104, Appl
52	14.4	1.6	17	1	US-09-863-086-102	Sequence 102, Appl
53	14.4	1.6	17	1	US-09-863-086-104	Sequence 104, Appl
54	14.4	1.6	17	1	US-09-696-791-1547	Sequence 1547, Ap
55	14	1.6	19	1	US-08-373-124A-962	Sequence 962, Appl
56	14	1.6	17	1	US-08-373-124A-964	Sequence 964, Appl
57	14	1.6	17	1	US-08-373-124A-966	Sequence 966, Appl
58	14	1.6	17	1	US-08-435-628-962	Sequence 962, Appl
59	14	1.6	17	1	US-08-435-628-964	Sequence 964, Appl
60	14	1.6	17	1	US-08-435-628-966	Sequence 966, Appl
61	13.8	1.6	17	1	US-08-584-040-5950	Sequence 5950, Ap
62	13.8	1.6	17	1	US-09-371-772B-2787	Sequence 2787, Ap
63	13.8	1.6	17	1	US-09-371-772B-5100	Sequence 5100, Ap
64	13.8	1.6	17	1	US-09-371-772B-6796	Sequence 6796, Ap
65	13.8	1.6	17	1	US-09-866-108A-8960	Sequence 8960, Ap
66	13.8	1.6	17	1	US-09-685-664B-2787	Sequence 2787, Ap
67	13.8	1.6	18	1	US-08-379-081B-88	Sequence 88, Appl
68	13.8	1.6	18	1	US-08-379-081B-89	Sequence 89, Appl
69	13.8	1.6	18	1	US-08-379-081B-90	Sequence 90, Appl
70	13.8	1.6	18	1	US-08-379-081B-91	Sequence 91, Appl
71	13.8	1.6	18	1	US-08-379-081B-92	Sequence 92, Appl
72	13.8	1.6	18	1	US-08-379-081B-93	Sequence 93, Appl
73	13.8	1.6	18	1	US-08-379-081B-94	Sequence 94, Appl
74	13.8	1.6	18	1	US-08-379-081B-95	Sequence 95, Appl
75	13.8	1.6	18	1	US-08-379-081B-96	Sequence 96, Appl
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C 109	14.4	1.6	17	1	AX701183	ACCSSION:AX701183	182	13.4	1.5	15	1	CQ821404	ACCSSION:CQ821404
C 110	14.4	1.6	17	1	AX706656	ACCSSION:AX706656	183	13.4	1.5	15	1	CQ821409	ACCSSION:CQ821409
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Oct 6 10.

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
3.794 Million cell updates/sec

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Post-processing: Minimum Match 0%  
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Listing first 363 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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C 38	17.2	2.0	22	1	AR438965
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C 87	15	1.7	15	1	AR0821402
C 88	15	1.7	15	1	AR0821408
C 89	15	1.7	15	1	AX081871
C 90	15	1.7	17	1	AX706658
C 91	15	1.7	17	1	AX707588
C 92	15	1.7	17	1	AX732679
C 93	15	1.7	20	1	AR199396
C 94	14.8	1.7	19	1	BD195707
C 95	14.8	1.7	19	1	AR282800
C 96	14.8	1.7	19	1	AX129356
C 97	14.4	1.6	17	1	A16196
C 98	14.4	1.6	17	1	A16242
C 99	14.4	1.6	17	1	BD203207
C 100	14.4	1.6	17	1	BD255579
C 101	14.4	1.6	17	1	BD255582
C 102	14.4	1.6	17	1	BD257636
C 103	14.4	1.6	17	1	I23680
C 104	14.4	1.6	17	1	I23682
C 105	14.4	1.6	17	1	AR433547
C 106	14.4	1.6	17	1	AR433549

GenBank/EMBL



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 6, 2005, 10:38:15 ; Search time 0.001 Seconds  
(without alignments)  
218.500 Million cell updates/sec

Title: US-10-633-843-3-COPY  
Perfect score: 874  
Sequence: 1 ctgcgagctcgtgggtttcc.....tattaaagaatccaattc 874

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 0.5

Searched: 4 seqs, 125 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 5 summaries

Database : estdb.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	42.4	4.9	48	1	N79542 ACCESSION:N79542
C 2	36	4.1	44	1	H41186 ACCESSION:H41186
C 3	14.8	1.7	19	1	AZ610584 ACCESSION:AZ610584
C 4	11.8	1.4	44	1	H41186 ACCESSION:H41186
C 5	10.8	1.2	14	1	AJ590269 ACCESSION:AJ590269

#### ALIGNMENTS

RESULT 1  
N79542/c  
LOCUS  
DEFINITION  
IMAGE:301607.3' similar to gb:X02317 SUPEROXIDE DISMUTASE (HUMAN);  
mRNA sequence.  
ACCESSION  
N79542  
VERSION  
N79542.1 GI:1242243  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 48)  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.  
TITLE  
The WashU-Merck EST Project  
JOURNAL  
Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1582  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Trace considered overall: poor quality  
Seq primer: ml3 -40 forward  
High quality sequence stop: 1.

#### FEATURES

source

1..48  
Location/Qualifiers

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1246531"  
/db\_xref="taxon:9606"  
/clone="IMAGE:301607"  
/dev\_stage="19 weeks"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_lib="Soares fetal lung NBHL19W"  
/note="Organ: lung; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; let strand cDNA was primed with a Not I - oligo(dT) primer [5'-TGTTACCAATCTGAGTGGAGCGCCGCAATTTTCTTTT-3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by Bento Soares and M. Patricia Bonaldo. This library was constructed from the same fetus as the fetal heart library, Soares fetal heart NBHL19W."

Query Match 4.9%; Score 42.4; DB 1; Length 48;  
Best Local Similarity 89.6%; Pred. No. 0.18;  
Matches 43; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 533 TTCCCTTGATCTAGTCTGAGGCCCTTAACATCTGTATCTCTCT 580

Db 48 TTCCCTNGTGTAGTCTGAGGCCCTTACNCATCTGTCTCTCT 1

#### RESULT 2

H41186  
LOCUS  
DEFINITION  
IMAGE:175485.5' similar to gb:X02317 SUPEROXIDE DISMUTASE (HUMAN);  
mRNA sequence.  
ACCESSION  
H41186  
VERSION  
H41186.1 GI:917238  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 44)  
AUTHORS  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawkins, M., Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F., Trevisan, E., Waterston, R., Williamson, A., Wohlmann, P., and Wilson, R.  
TITLE  
The WashU-Merck EST Project  
JOURNAL  
Unpublished (1995)  
COMMENT  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
Insert Size: 1582  
High quality sequence starts: 1  
High quality sequence stops: 1  
Source: IMAGE Consortium, LLNL  
This clone is available royalty-free through LLNL ; contact the